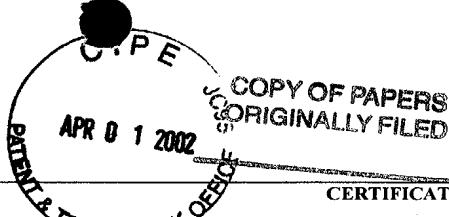


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Typed or Printed Name      Donna Macedo

Signature      *Donna Macedo*

Date      3/19/02

RESPONSE		Application Number	09/398,399
		Attorney Docket Number	10981620-2
		Filing Date	September 17, 1999
		First Named Inventor	Delenstarr
		Examiner	Sisson, B.
		Group Art	1655
		Title	Techniques for Assessing Nonspecific Binding of Nucleic Acids to Surfaces

Sir:

This amendment is responsive to the FINAL REJECTION dated December 19, 2001. In view of the amendments to the claims and the remarks put forth below, reconsideration and allowance are respectfully requested.

AMENDMENTS

In the specification:

Page 30, lines 23-29:

Hybridization conditions were as follows. The buffer consisted of 6×SSPE (sodium chloride/sodium phosphate/ethylenediamine tetra-acetic acid (EDTA)), 0.005% TRITON™X-100 (polyoxyethylene(10)isooctylphenyl ether), 0.1% w/v SDS (sodium dodecyl sulfate), 0.1% w/v BSA (bovine serum albumin, fraction V), 100 µg/ml hsDNA (heat-denatured herring sperm DNA). SSPE buffer components are described by Sambrook J. et al., in Molecular Cloning: A Laboratory Manual (Vol. 3, p. B13; 2nd Ed., 1989; Cold Spring Harbor Laboratory Press). The target, R6G-labeled G3PDH cRNA (SEQ ID NO:1), was present at 1 nm.

*F1*  
[ Page 31, lines 10 to 13: ]

Arrays were washed by first removing the hybridization target/buffer solution, flushing the hybridization chamber with 6×SSPE/0.005% TRITON™X-100 (polyoxyethylene(10)isooctylphenyl ether), disassembling the hybridization chamber, and

*John Hunter  
4/15/02  
BPL*

*F2*

*Fr  
cont*  
washing the array in a beaker of 0.1× SSPE/0.005% TRITON™X-100 (polyoxyethylene(10)isooctylphenyl ether) at room temperature for 15 minutes with mixing.

*F3*  
**In the claims:**

54. (Amended) The method according to Claim 50, wherein said method further comprises subtracting a detected signal, wherein said detected signal is from said at least one background feature, from signal detected from any other probe nucleic acid feature of said collection of substrate bound probe nucleic acid features.

**REMARKS**

**Formal Matters**

Claims 50 to 78 are pending after entry of the amendments set forth herein.

The above amendments to the specification address issues raised by the Examiner with respect to the use of the Triton X-100 and TX100 marks. Claim 54 has been amended merely to clarify the claim language. Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached is captioned "**VERSION WITH MARKINGS TO SHOW CHANGES MADE.**" Applicants respectfully request reconsideration of the application in view of the amendments and remarks made herein.

Claims 50 to 78 were rejected under 35 U.S.C. § 112, 2<sup>nd</sup> ¶ for a number of issues, each of which is addressed separately below.

The Examiner asserts that the claims are confusing with respect to the "whether all of the target nucleic acids are to be 14 bases in length and have 70% sequence identity with a probe, or whether target nucleic acids of some other length and percent identity can be used."

The claim language in question reads in relevant part:

contacting a sample of target nucleic acids **under hybridization conditions that require a target**

nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe.

The above language specifies the nature of the hybridization conditions, **not the nature of the targets or probes**. Specifically, the above language specifies that the hybridization conditions are ones that require a nucleic acid to be 14 nt long and to have at least 70% sequence identity with a probe nucleic acid in order for it to hybridize to a probe nucleic acid. The language clearly is not specifying anything about the particular targets or probes actually employed in the method, but is clearly specifying in a precise manner the nature of the hybridization conditions used in the methods. Since the language is clearly referring to the nature of the hybridization conditions, and not the nature of the probes or targets, the language is not indefinite and this rejection may be withdrawn.

With respect to the second issue regarding whether hybridization conditions that allow for targets with less homology to hybridize may be employed, again the claim language reads:

**under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe.**

It is readily apparent from the language that hybridization conditions that allow for hybridization when the 70% sequence identity parameter is not met are not included within the suitable hybridization conditions.

With respect to the term "minimally," the patent law only requires that a term employed in claim be clear to those of skill in the art when read in view of the specification. The specification at page 21, lines 25 ff provides a description of what this term means as this term is employed in the claims. Furthermore, several specific instances of "minimally binding nucleic acids," are provided in the Experimental Section. As such, this term is not ambiguous to one of skill in the art when read in view of the specification.

With respect to the term "selectively" as employed in the claims, when read in view of the specification this term clearly is ascribed in the claims as having the same meaning as "specifically," since the claims refer to the background probes as not selectively hybridizing to target and the background probes are defined in the specification as ones that do not

Atty Dkt. No.: 10981620-2  
USSN: 09/398,399

specifically hybridize to target nucleic acids. See page 15, lines 18 ff. The phrase "specifically hybridizes" is also clearly defined in the specification at page 9, lines 25 ff.

Finally, with respect to Claim 54, in view of the above amendments to Claim 54, it is submitted that the language of this claim is clear with respect to the fact that the detected signal is not subtracted from a background signal, but is the background signal.

In sum, in view of the above remarks and amendments, the rejections of the claims under 35 U.S.C. § 112, 2<sup>nd</sup> ¶ may be withdrawn.

### Conclusion

The applicant respectfully submits that all of the claims are in condition for allowance, which action is requested. If the Examiner finds that a telephone conference would expedite the prosecution of this application, please telephone Gordon Stewart at 650 485 2386. The Commissioner is hereby authorized to charge any fees under 37 C.F.R. §§ 1.16 and 1.17 which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-1078.

Respectfully submitted,

Date: 3.19.02

By:   
Bret E. Field  
Registration No. 37,620



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

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Page 31, lines 10 to 13:

Arrays were washed by first removing the hybridization target/buffer solution, flushing the hybridization chamber with 6×SSPE/0.005% TX100 TRITON™X-100 (polyoxyethylene(10)isooctylphenyl ether), disassembling the hybridization chamber, and washing the array in a beaker of 0.1× SSPE/0.005% TX100 TRITON™X-100 (polyoxyethylene(10)isooctylphenyl ether) at room temperature for 15 minutes with mixing.

In the claims:

54. (Amended) The method according to Claim 50, wherein said method further comprises subtracting a detected signal, wherein said detected signal is from said at least one background feature, from signal detected from any other probe nucleic acid feature of said collection of substrate bound probe nucleic acid features.